



PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/501,282

DATE: 07/20/2004
TIME: 11:37:49

Input Set : D:\Aml00780.app
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3 <110> APPLICANT: MCMICHAEL, JOHN CALHOON
 4 ZAGURSKY, ROBERT JOHN
 5 RUSSELL, DAVID PARRISH
 6 FLETCHER, LEAH DIANE
 8 <120> TITLE OF INVENTION: ALLOIOCOCCUS OTITIDIS OPEN READING FRAMES (ORFS) ENCODING
 9 POLYPEPTIDE ANTIGENS, IMMUNOGENIC COMPOSITIONS AND USES THEREOF
 11 <130> FILE REFERENCE: AM100780 L2
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/501,282
 C--> 14 <141> CURRENT FILING DATE: 2004-07-09
 16 <150> PRIOR APPLICATION NUMBER: 60/333,777
 17 <151> PRIOR FILING DATE: 2001-11-29
 19 <150> PRIOR APPLICATION NUMBER: 60/426,742
 20 <151> PRIOR FILING DATE: 2002-11-18
 22 <150> PRIOR APPLICATION NUMBER: PCT/US02/36123
 23 <151> PRIOR FILING DATE: 2002-11-25
 25 <160> NUMBER OF SEQ ID NOS: 6653
 27 <170> SOFTWARE: PatentIn version 3.2
 29 <210> SEQ ID NO: 1
 30 <211> LENGTH: 870
 31 <212> TYPE: DNA
 32 <213> ORGANISM: Alloioococcus otitidis
 34 <220> FEATURE:
 35 <221> NAME/KEY: CDS
 36 <222> LOCATION: (4)..(867)
 38 <400> SEQUENCE: 1
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 40 Met Met Asp Glu Arg Leu Thr Ser Leu Leu Gly Ile Ser Tyr Pro
 41 1 5 10 15
 43 att att caa ggc gga atg gcg aag att tcc aga cct gac ctg gtt tct 96
 44 Ile Ile Gln Gly Gly Met Ala Lys Ile Ser Arg Pro Asp Leu Val Ser
 45 20 25 30
 47 gcc gtg agt caa gcg ggt ggc ttg ggt gtt ttg acc tcc atg ggg ctg 144
 48 Ala Val Ser Gln Ala Gly Gly Leu Gly Val Leu Thr Ser Met Gly Leu
 49 35 40 45
 51 act ccc caa gag ttg agc cag gat atc cag gaa gtc caa aag cgg att 192
 52 Thr Pro Gln Glu Leu Ser Gln Asp Ile Gln Glu Val Gln Lys Arg Ile
 53 50 55 60
 55 gat cag ccc ttt gcc gtc aac cta atg ctc cag caa gat aat att ttt 240
 56 Asp Gln Pro Phe Ala Val Asn Leu Met Leu Gln Gln Asp Asn Ile Phe
 57 65 70 75
 59 gac ctc ctg gaa gtg atc aaa gaa gtg aaa ccc cct gtg gtg atg acc 288
 60 Asp Leu Leu Glu Val Ile Lys Glu Val Lys Pro Pro Val Val Met Thr
 61 80 85 90 95

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63	ggt gct ggc agt ccc aaa gct ttt gtc caa gat tta agg gat ttg gac	336
64	Gly Ala Gly Ser Pro Lys Ala Phe Val Gln Asp Leu Arg Asp Leu Asp	
65	100 105 110	
67	atc aag gtc atc cca gtc ctg tcg acg gtg agc cag gcc cag aaa atg	384
68	Ile Lys Val Ile Pro Val Leu Ser Thr Val Ser Gln Ala Gln Lys Met	
69	115 120 125	
71	gaa gcc tta ggg gtg gat gcc atc gta gta gaa ggt caa gaa gca ggt	432
72	Glu Ala Leu Gly Val Asp Ala Ile Val Val Glu Gly Gln Glu Ala Gly	
73	130 135 140	
75	ggt cac att ggt tgg acg tca acc atg gct agc ctg ccc cag gtg gtc	480
76	Gly His Ile Gly Trp Thr Ser Thr Met Ala Ser Leu Pro Gln Val Val	
77	145 150 155	
79	cag gct gtt gac att ccg gtt gta gcg gca ggc ggt atc ggg tca gga	528
80	Gln Ala Val Asp Ile Pro Val Val Ala Ala Gly Gly Ile Gly Ser Gly	
81	160 165 170 175	
83	cag gcc att gca gca gcg gaa tgt ctg gga gct tgt ggt gtt cag ttg	576
84	Gln Ala Ile Ala Ala Glu Cys Leu Gly Ala Cys Gly Val Gln Leu	
85	180 185 190	
87	ggg acc ttg ttt ttg tcg gct aaa gaa tgc ccc atc agt gac ctc tac	624
88	Gly Thr Leu Phe Leu Ser Ala Lys Glu Cys Pro Ile Ser Asp Leu Tyr	
89	195 200 205	
91	cgc aaa aaa tta ctg gcc tgc cag gac cag gac acc ctg gtt agt gaa	672
92	Arg Lys Lys Leu Leu Ala Cys Gln Asp Gln Asp Thr Leu Val Ser Glu	
93	210 215 220	
95	ctc cac ccg ggt ggc cggtt ggtt ggtt ggtt ggtt ggtt ggtt ggtt ggtt	720
96	Leu His Pro Gly Gly Arg Val Arg Ser Leu Lys Ala Ser Cys Gln Asp	
97	225 230 235	
99	gac cct gac ctc ttg gcc aag gaa ggg gaa gcc ggc ctc cat tat gcc	768
100	Asp Pro Asp Leu Leu Ala Lys Glu Gly Glu Ala Gly Leu His Tyr Ala	
101	240 245 250 255	
103	ggg gaa gtg gca gga caa ata gac aat tta gcc aca gca gaa att	816
104	Gly Glu Val Ala Gly Gln Ile Asp Asn Leu Ala Thr Ala Gln Glu Ile	
105	260 265 270	
107	gta gac cga ctt gta gcc caa tac caa tcg aca cta aaa aaa cta att	864
108	Val Asp Arg Leu Val Ala Gln Tyr Gln Ser Thr Leu Lys Lys Leu Ile	
109	275 280 285	
111	caa taa	870
112	Gln	
115	<210> SEQ ID NO: 2	
116	<211> LENGTH: 288	
117	<212> TYPE: PRT	
118	<213> ORGANISM: Alloioiococcus otitidis	
120	<400> SEQUENCE: 2	
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122	1 5 10 15	
124	Ile Gln Gly Gly Met Ala Lys Ile Ser Arg Pro Asp Leu Val Ser Ala	
125	20 25 30	
127	Val Ser Gln Ala Gly Gly Leu Gly Val Leu Thr Ser Met Gly Leu Thr	
128	35 40 45	

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130 Pro Gln Glu Leu Ser Gln Asp Ile Gln Glu Val Gln Lys Arg Ile Asp
131 50 55 60
133 Gln Pro Phe Ala Val Asn Leu Met Leu Gln Gln Asp Asn Ile Phe Asp
134 65 70 75 80
136 Leu Leu Glu Val Ile Lys Glu Val Lys Pro Pro Val Val Met Thr Gly
137 85 90 95
139 Ala Gly Ser Pro Lys Ala Phe Val Gln Asp Leu Arg Asp Leu Asp Ile
140 100 105 110
142 Lys Val Ile Pro Val Leu Ser Thr Val Ser Gln Ala Gln Lys Met Glu
143 115 120 125
145 Ala Leu Gly Val Asp Ala Ile Val Val Glu Gly Gln Glu Ala Gly Gly
146 130 135 140
148 His Ile Gly Trp Thr Ser Thr Met Ala Ser Leu Pro Gln Val Val Gln
149 145 150 155 160
151 Ala Val Asp Ile Pro Val Val Ala Ala Gly Gly Ile Gly Ser Gly Gln
152 165 170 175
154 Ala Ile Ala Ala Ala Glu Cys Leu Gly Ala Cys Gly Val Gln Leu Gly
155 180 185 190
157 Thr Leu Phe Leu Ser Ala Lys Glu Cys Pro Ile Ser Asp Leu Tyr Arg
158 195 200 205
160 Lys Lys Leu Leu Ala Cys Gln Asp Gln Asp Thr Leu Val Ser Glu Leu
161 210 215 220
163 His Pro Gly Gly Arg Val Arg Ser Leu Lys Ala Ser Cys Gln Asp Asp
164 225 230 235 240
166 Pro Asp Leu Leu Ala Lys Glu Gly Glu Ala Gly Leu His Tyr Ala Gly
167 245 250 255
169 Glu Val Ala Gly Gln Ile Asp Asn Leu Ala Thr Ala Gln Glu Ile Val
170 260 265 270
172 Asp Arg Leu Val Ala Gln Tyr Gln Ser Thr Leu Lys Lys Leu Ile Gln
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176 <210> SEQ ID NO: 3
177 <211> LENGTH: 957
178 <212> TYPE: DNA
179 <213> ORGANISM: Alloioiococcus otitidis
181 <220> FEATURE:
182 <221> NAME/KEY: CDS
183 <222> LOCATION: (85)..(954)
185 <400> SEQUENCE: 3
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189 cagtacccaa ttatccaggg tggg atg gcc cggtt att agt aag cca gaa tta 111
190 Met Ala Arg Ile Ser Lys Pro Glu Leu
191 1 5
193 gtc agt gct gtc agt gca ggt ggc cta ggc gtt tta acc tcg gtt 159
194 Val Ser Ala Val Ser Ala Gly Gly Leu Gly Val Leu Thr Ser Val
195 10 15 20 25
197 ggg gtg gat gca gcg ggt ttt cgg gcg gac atc cag gaa atc cgc cgt 207
198 Gly Val Asp Ala Ala Gly Phe Arg Ala Asp Ile Gln Glu Ile Arg Arg
199 30 35 40
201 ttg acg gac aag ccc ttt ggg gtc aac ttg atg ttg cag ttg gac aac 255

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202	Leu	Thr	Asp	Lys	Pro	Phe	Gly	Val	Asn	Leu	Met	Leu	Gln	Leu	Asp	Asn		
203					45					50					55			
205	att	cct	gaa	ttg	ttg	gag	gtt	gtc	aag	gaa	aaa	cca	gcc	gtt	gtc		303	
206	Ile	Pro	Glu	Leu	Leu	Glu	Val	Val	Lys	Glu	Glu	Lys	Pro	Ala	Val	Val		
207					60				65					70				
209	tta	act	gga	gcg	ggg	acc	ccg	aaa	gac	ttt	gcc	caa	gac	ttg	caa	gca		
210	Leu	Thr	Gly	Ala	Gly	Thr	Pro	Lys	Asp	Phe	Ala	Gln	Asp	Leu	Gln	Ala	351	
211					75				80					85				
213	ctt	ggc	atc	aaa	gtt	atc	ccg	gtt	gtc	tct	gcc	gtc	aag	cat	gcc	aag	399	
214	Leu	Gly	Ile	Lys	Val	Ile	Pro	Val	Val	Ser	Ala	Val	Lys	His	Ala	Lys		
215	90					95				100					105			
217	aaa	atg	gaa	gcc	ttg	ggt	gtg	gat	gcc	gtt	gtt	gaa	ggc	caa	gaa		447	
218	Lys	Met	Glu	Ala	Leu	Gly	Val	Asp	Ala	Val	Val	Cys	Glu	Gly	Gln	Glu		
219						110				115					120			
221	gct	ggt	ggt	cac	att	ggg	atc	act	tct	acc	atg	gcc	acc	ctg	ccc	cag		
222	Ala	Gly	Gly	His	Ile	Gly	Ile	Thr	Ser	Thr	Met	Ala	Thr	Leu	Pro	Gln	495	
223						125				130					135			
225	gtg	gtg	caa	gct	gtt	gat	atg	cca	gtt	att	gct	gct	ggt	gga	atc	ggg		
226	Val	Val	Gln	Ala	Val	Asp	Met	Pro	Val	Ile	Ala	Ala	Gly	Gly	Ile	Gly	543	
227						140				145					150			
229	tca	ggc	cag	gcc	att	gct	gca	gca	gaa	tgt	tta	ggg	gca	tgc	ggg	gta		
230	Ser	Gly	Gln	Ala	Ile	Ala	Ala	Ala	Glu	Cys	Leu	Gly	Ala	Cys	Gly	Val	591	
231						155				160					165			
233	caa	ata	ggg	acc	ttg	ttt	ttg	gca	gca	gaa	gag	tgt	gcc	att	agc	gag		
234	Gln	Ile	Gly	Thr	Leu	Phe	Leu	Ala	Ala	Glu	Glu	Cys	Ala	Ile	Ser	Glu		
235	170					175				180					185			
237	gcc	tac	cgc	cag	cag	gtc	att	gat	gct	ggc	gac	caa	gat	acc	att	gtt		
238	Ala	Tyr	Arg	Gln	Gln	Val	Ile	Asp	Ala	Gly	Asp	Gln	Asp	Thr	Ile	Val	687	
239						190				195					200			
241	acc	gga	att	agt	acc	ggt	ggc	cg	gtc	agg	tcc	gtt	gcc	tct	cct	ttc		
242	Thr	Gly	Ile	Ser	Thr	Gly	Gly	Arg	Val	Arg	Ser	Val	Ala	Ser	Pro	Phe		
243						205				210					215			
245	ttg	gct	gaa	ctc	ttg	gcc	gat	gaa	tta	aag	ggg	tta	gac	cct	aaa	gtt		
246	Leu	Ala	Glu	Leu	Ala	Asp	Glu	Leu	Lys	Gly	Leu	Asp	Pro	Lys	Val		783	
247						220				225					230			
249	tcc	ttg	gaa	agg	act	caa	gga	tct	tat	gdc	cg	gcc	att	gcc	gga	gaa		
250	Phe	Leu	Glu	Arg	Thr	Gln	Gly	Ser	Tyr	Gly	Arg	Ala	Ile	Ala	Gly	Glu		
251						235				240					245			
253	att	gac	caa	ggg	acc	atc	cag	gct	ggc	gaa	gta	gca	ggt	caa	gtt	aaa		
254	Ile	Asp	Gln	Gly	Thr	Ile	Gln	Ala	Gly	Glu	Val	Ala	Gly	Gln	Val	Lys		
255	250					255				260					265			
257	gcc	aag	tct	act	gcc	aaa	gca	atc	att	gac	cg	ctc	gtg	gct	gaa	tac		
258	Ala	Lys	Ser	Thr	Ala	Lys	Ala	Ile	Ile	Asp	Arg	Leu	Val	Ala	Glu	Tyr		
259						270				275					280			
261	cag	gaa	acc	gta	gcc	aag	ttt	cag	agt	taa							957	
262	Gln	Glu	Thr	Val	Ala	Lys	Phe	Gln	Ser									
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268 <212> TYPE: PRT
 269 <213> ORGANISM: Alloioococcus otitidis
 271 <400> SEQUENCE: 4
 272 Met Ala Arg Ile Ser Lys Pro Glu Leu Val Ser Ala Val Ser Ser Ala
 273 1 5 10 15
 276 Gly Gly Leu Gly Val Leu Thr Ser Val Gly Val Asp Ala Ala Gly Phe
 277 20 25 30
 280 Arg Ala Asp Ile Gln Glu Ile Arg Arg Leu Thr Asp Lys Pro Phe Gly
 281 35 40 45
 284 Val Asn Leu Met Leu Gln Leu Asp Asn Ile Pro Glu Leu Leu Glu Val
 285 50 55 60
 288 Val Lys Glu Glu Lys Pro Ala Val Val Leu Thr Gly Ala Gly Thr Pro
 289 65 70 75 80
 292 Lys Asp Phe Ala Gln Asp Leu Gln Ala Leu Gly Ile Lys Val Ile Pro
 293 85 90 95
 296 Val Val Ser Ala Val Lys His Ala Lys Lys Met Glu Ala Leu Gly Val
 297 100 105 110
 300 Asp Ala Val Val Cys Glu Gly Gln Glu Ala Gly Gly His Ile Gly Ile
 301 115 120 125
 304 Thr Ser Thr Met Ala Thr Leu Pro Gln Val Val Gln Ala Val Asp Met
 305 130 135 140
 308 Pro Val Ile Ala Ala Gly Gly Ile Gly Ser Gly Gln Ala Ile Ala Ala
 309 145 150 155 160
 312 Ala Glu Cys Leu Gly Ala Cys Gly Val Gln Ile Gly Thr Leu Phe Leu
 313 165 170 175
 316 Ala Ala Glu Glu Cys Ala Ile Ser Glu Ala Tyr Arg Gln Gln Val Ile
 317 180 185 190
 320 Asp Ala Gly Asp Gln Asp Thr Ile Val Thr Gly Ile Ser Thr Gly Gly
 321 195 200 205
 324 Arg Val Arg Ser Val Ala Ser Pro Phe Leu Ala Glu Leu Leu Ala Asp
 325 210 215 220
 328 Glu Leu Lys Gly Leu Asp Pro Lys Val Phe Leu Glu Arg Thr Gln Gly
 329 225 230 235 240
 332 Ser Tyr Gly Arg Ala Ile Ala Gly Glu Ile Asp Gln Gly Thr Ile Gln
 333 245 250 255
 336 Ala Gly Glu Val Ala Gly Gln Val Lys Ala Lys Ser Thr Ala Lys Ala
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 341 275 280 285
 344 Gln Ser
 345 290
 348 <210> SEQ ID NO: 5
 349 <211> LENGTH: 957
 350 <212> TYPE: DNA
 351 <213> ORGANISM: Alloioococcus otitidis
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 354 <221> NAME/KEY: CDS
 355 <222> LOCATION: (25)..(954)
 357 <400> SEQUENCE: 5

VERIFICATION SUMMARY

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Input Set : D:\Am100780.app

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L:13 M:270 C: Current Application Number differs, Replaced Application Number

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date